lassoRegCOVID.R

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```
library(readxl)
## Warning: package 'readxl' was built under R version 4.0.3
library(glmnet)
## Warning: package 'glmnet' was built under R version 4.0.4
## Loading required package: Matrix
## Loaded glmnet 4.1-1
library(tidyverse)
## Warning: package 'tidyverse' was built under R version 4.0.3
## -- Attaching packages ------ tidyverse 1.3.0 --
## v ggplot2 3.3.3 v purrr 0.3.4

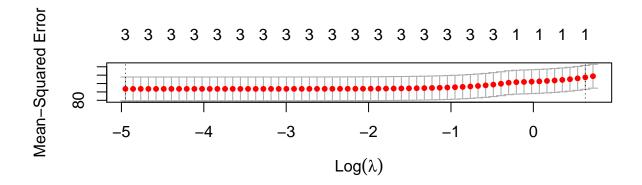
## v tibble 3.1.0 v dplyr 1.0.5

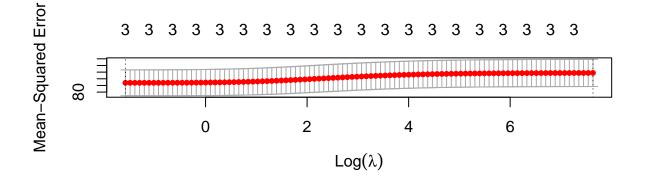
## v tidyr 1.1.3 v stringr 1.4.0

## v readr 1.4.0 v forcats 0.5.1
## Warning: package 'ggplot2' was built under R version 4.0.3
## Warning: package 'tibble' was built under R version 4.0.4
## Warning: package 'tidyr' was built under R version 4.0.4
## Warning: package 'readr' was built under R version 4.0.3
## Warning: package 'purrr' was built under R version 4.0.3
## Warning: package 'dplyr' was built under R version 4.0.4
## Warning: package 'stringr' was built under R version 4.0.3
```

```
## Warning: package 'forcats' was built under R version 4.0.3
## -- Conflicts ----- tidyverse_conflicts() --
## x tidyr::expand() masks Matrix::expand()
## x dplyr::filter() masks stats::filter()
## x dplyr::lag()
                    masks stats::lag()
## x tidyr::pack() masks Matrix::pack()
## x tidyr::unpack() masks Matrix::unpack()
library(caret)
## Warning: package 'caret' was built under R version 4.0.3
## Loading required package: lattice
##
## Attaching package: 'caret'
## The following object is masked from 'package:purrr':
##
##
      lift
data = read_xlsx("C:\\Users\\91828\\Documents\\Rlab\\Covid\\Rgeression-Model-Dataset.xlsx")
# view(data)
# Load the data and remove NAs
data <- na.omit(data)</pre>
# Split the data into training and test set
set.seed(123)
training.samples <- data$positivity_rate %>%
  createDataPartition(p = 0.8, list = FALSE)
train.data <- data[training.samples, ]</pre>
test.data <- data[-training.samples, ]</pre>
# levels of each var[Taking only predictors with level>=2]
# map(map(train.data, as.factor), levels)
train.data <- train.data[map(map(train.data,as.factor),levels),length)>1]
test.data <- test.data[map(map(map(test.data,as.factor),levels),length)>1]
# Dumy code categorical predictor variables
x <- model.matrix(positivity_rate ~testing_rate+population+new_cases , train.data)
# Convert the outcome (class) to a numerical variable
y <- train.data$positivity_rate
# Find the best lambda using cross-validation
set.seed(123)
```

```
cv.lasso <- cv.glmnet(x, y, alpha = 1)
cv.ridge <- cv.glmnet(x, y, alpha = 0)
par(mfrow=c(2,1))
plot(cv.lasso)
plot(cv.ridge)</pre>
```





coef(model.ridge)

```
## 5 x 1 sparse Matrix of class "dgCMatrix"
## s0
## (Intercept) 7.494487e+00
## (Intercept) .
## testing_rate -1.007731e-06
## population 6.282534e-13
## new_cases 4.693890e-07

#FEVER, TIREDNESS DRYCOUGH SORETHROAT NONESYMPTON are most significant according to lasso.
#Whereas RIDGE includes all the parameters
# Make predictions on the test data LASSO
x.test <- model.matrix(positivity_rate~testing_rate+population+new_cases,test.data)[,-1]</pre>
```